

SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.

<120> METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING GYRASE GENE AS  
AN INDICATOR

<130> PH-581

<140> US09/208, 688

<141> 1998-12-10

<150> JP97/343316

<151> 1997-12-12

<160> 80

<170> PatentIn version 2.0

<210> 1

<211> 1212

<212> DNA

<213> Bacteroides vulgatus

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<221> CDS

<222> (1)... (1212)

<400> 1

09222222-033001

09823829.033004

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Ser Cys Val Asn Ala Leu Ser Thr His Met Thr Thr Gln Val Phe Arg	
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Ser Val Lys Glu Val Gly Thr Ala Asp Ile Thr Gly Thr Lys Gln Thr	
50 55 60	
ttc tgg ccg gat gat acc atc ttc act gtt acc gaa tat aag ttt gac	240
Phe Trp Pro Asp Asp Thr Ile Phe Thr Val Thr Glu Tyr Lys Phe Asp	
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att cta cag gca cgt atg cgt gaa ttg gcc tac ttg aac aaa ggt atc	288
Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile	
85 90 95	
acc att tca ctg acc gac cgc cgg atc aaa gaa gaa gat ggc agc ttc	336
Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe	
100 105 110	
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Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg	
115 120 125	
ttc ctg aac cgt aac aac gaa gcg ctg att aat gat gtc att tat ctg	432
Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu	
130 135 140	
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Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn	

145	150	155	160	
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Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr				
165	170	175		
ata gaa ggc ggt aca cac gag gcc ggt ttc cgc agc gca tta acc cgt	576			
Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg				
180	185	190		
gta ctg aag aaa tat gcg gaa gat acc aaa gca ctg gaa aaa gca aaa	624			
Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys				
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Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile				
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ctg ggc aac agc gaa gtg agt ggt gcc gtg aac caa gct gta ggc gaa	768			
Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu				
245	250	255		
gcg ctt aca tat tat ctg gaa gaa cat ccg aaa gaa gca aaa cag att	816			
Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile				
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gtt gac aaa gtg atc ctg gct gca aca gcg cgt atc gcc gca cgc aag	864			
Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys				
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Phe	Trp	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Val	Thr	Glu	Tyr	Lys	Phe	Asp	
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Ile	Leu	Gln	Ala	Arg	Met	Arg	Glu	Leu	Ala	Tyr	Leu	Asn	Lys	Gly	Ile	
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Thr	Ile	Ser	Leu	Thr	Asp	Arg	Arg	Ile	Lys	Glu	Glu	Asp	Gly	Ser	Phe	
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Lys	Lys	Glu	Ile	Phe	His	Ser	Asp	Glu	Gly	Val	Lys	Glu	Phe	Val	Arg	
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Phe	Leu	Asn	Arg	Asn	Asn	Glu	Ala	Leu	Ile	Asn	Asp	Val	Ile	Tyr	Leu	
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[illegible][illegible]







[illegible]

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Arg	Asp	Gly	Tyr	Glu	Trp	Phe	Gln	Tyr	Tyr	Asp	Arg	Ala	Val	Pro	Gly
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Thr	Leu	Lys	Gln	Gly	Glu	Ala	Thr	Lys	Lys	Thr	Gly	Thr	Thr	Ile	Arg
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Phe	Trp	Ala	Asp	Pro	Glu	Ile	Phe	Glu	Thr	Thr	Gln	Tyr	Asp	Phe	Glu
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Thr	Val	Ala	Arg	Arg	Leu	Gln	Glu	Met	Ala	Phe	Leu	Asn	Lys	Gly	Leu
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Thr	Ile	Asn	Leu	Thr	Asp	Glu	Arg	Val	Glu	Gln	Asp	Glu	Val	Val	Asp
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Glu	Val	Val	Ser	Asp	Thr	Ala	Glu	Ala	Pro	Lys	Ser	Ala	Glu	Glu	Gln
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Ala	Ala	Glu	Ser	Ala	Lys	Pro	His	Lys	Val	Lys	His	Arg	Thr	Phe	His
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Tyr	Pro	Gly	Gly	Leu	Val	Asp	Phe	Val	Lys	His	Ile	Asn	Arg	Thr	Lys
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260	265	270	
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe			
275	280	285	
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser			
290	295	300	
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg			
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Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp			
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Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly			
340	345	350	
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln			
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Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala			
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<212> DNA

<213> Chitinophaga pinensis

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<221> CDS

<222> (1)... (660)

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15

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20

25

30

gac ttc cgt gaa ggt ctg agc gct atc atc agc gta aaa gta cct gaa 144

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35

40

45

cca cag ttc gaa ggc cag acc aaa acc aaa ctc ggt aac tcc gat gta 192

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50

55

60

atg ggg gtt gtg gac agt tcc gta gca gcc gta ctg gat gcc tac ctg 240

Met Gly Val Val Asp Ser Ser Val Ala Ala Val Leu Asp Ala Tyr Leu

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70

75

80

gaa gaa cat ccc cgc gaa gcc aag atc att atc aat aaa gtg gta ctg 288

Glu Glu His Pro Arg Glu Ala Lys Ile Ile Ile Asn Lys Val Val Leu

85

90

95

gca gca cag gcg cgt gaa gca gcc cgt aaa gca cgc cag atg gta cag 336

Ala Ala Gln Ala Arg Glu Ala Ala Arg Lys Ala Arg Gln Met Val Gln

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cgt aag agc gta ctg agt gga agc ggc ttg cct ggt aaa ctg gct gac			384
Arg Lys Ser Val Leu Ser Gly Ser Gly Leu Pro Gly Lys Leu Ala Asp			
115	120	125	
tgc tct gaa aat gat cct gaa aaa tgt gaa ctg tac ctg gta gag ggt			432
Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly			
130	135	140	
gac tcc gca ggt ggt acg gct aaa caa gga cgt aac cgt agc ttc cag			480
Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln			
145	150	155	160
gcg atc ctg ccg ctc agg ggt aaa atc ctg aac gtg gag aaa gcc atg			528
Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met			
165	170	175	
gag cat aag ata tat gag aat gag gag att aaa aac atc ttc acc gca			576
Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala			
180	185	190	
ctt ggt gta acc atc ggt acg gaa gaa gat gac aaa gcc ctc aac ctc			624
Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu			
195	200	205	
tcc aaa ctg cgc tat cac aaa ctg atc atc atg acg			660
Ser Lys Leu Arg Tyr His Lys Leu Ile Ile Met Thr			
210	215	220	

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<211> 220

<212> PRT

<213> Chitinophaga pinensis

<400> 6





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115 120 125  
cga ttt ita gat gct ggt aga gaa cca att att tct cac gta ata agc 432  
Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser  
130 135 140  
atg gag cac gaa aaa gga gaa gtt cct gtt gag gtt gct ctt gtt tac 480  
Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr  
145 150 155 160  
aat aca agt tac tcc gaa aat att ttc tct tac gta aat aat att aac 528  
Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn  
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Thr His Glu

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<213> Flavobacterium aquatile

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35 40 45



Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr

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55

60

Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr

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70

75

80

Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly

85

90

95

Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp

100

105

110

Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val

115

120

125

Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser

130

135

140

Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr

145

150

155

160

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170

175

Thr His Glu

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<213> Mycobacterium asiaticum

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Arg	Asp	Gly	His	Glu	Trp	Phe	Gln	Tyr	Tyr	Asp	Arg	Ala	Val	Pro	Gly
		35				40						45			
Thr	Leu	Lys	Gln	Gly	Glu	Ala	Thr	Lys	Lys	Thr	Gly	Thr	Thr	Ile	Arg
	50					55						60			
Phe	Trp	Ala	Asp	Pro	Glu	Ile	Phe	Glu	Thr	Thr	Gln	Tyr	Asp	Phe	Glu
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Thr	Val	Ala	Arg	Arg	Leu	Gln	Glu	Met	Ala	Phe	Leu	Asn	Lys	Gly	Leu
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Thr	Ile	Asn	Leu	Thr	Asp	Glu	Arg	Val	Glu	Gln	Asp	Glu	Val	Val	Asp
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Glu	Val	Val	Ser	Asp	Thr	Ala	Glu	Ala	Pro	Lys	Ser	Ala	Glu	Glu	Lys
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Ala	Ala	Glu	Ser	Thr	Ala	Pro	His	Lys	Val	Lys	His	Arg	Thr	Phe	His
	130					135						140			
Tyr	Pro	Gly	Gly	Leu	Val	Asp	Phe	Val	Lys	His	Ile	Asn	Arg	Thr	Lys
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Ser	Pro	Ile	Gln	Gln	Ser	Val	Ile	Asp	Phe	Asp	Gly	Lys	Gly	Thr	Gly
			165					170					175		
His	Glu	Val	Glu	Ile	Ala	Met	Gln	Trp	Asn	Gly	Gly	Tyr	Ser	Glu	Ser
		180						185					190		
Val	His	Thr	Phe	Ala	Asn	Thr	Ile	Asn	Thr	His	Glu	Gly	Gly	Thr	His
		195						200					205		
Glu	Glu	Gly	Phe	Arg	Ser	Ala	Leu	Thr	Ser	Val	Val	Asn	Lys	Tyr	Ala
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[illegible]

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1 5 10 15	
gaa cta ata gaa ggc gga cac gtt tac ata gca aca cca cct tta tat	96
Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr	
20 25 30	
tta gtt aaa aaa gga act aaa aag cgt tat gct tgg aat gat aaa gaa	144
Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu	
35 40 45	
cga gat gaa ata gca gat agc ttt aat ggt agt gta ggt atc caa aga	192
Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg	
50 55 60	
tat	195

Tyr

65

<210> 12

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<212> PRT

<213> *Cytophaga lytica*

<400> 12

Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg

1

5

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15

Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr

20

25

30

Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu

35

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45

Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg

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55

60

Tyr

65

<210> 13

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Ile	Asp	Val	Arg	Leu	Leu	Lys	Asp	Gly	Ser	Cys	Gln	Val	Thr	Asp	Asn	
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ctc	gaa	acc	gtg	ctg	acg	att	ctg	cac	gcg	ggc	ggc	aag	ttt	ggc	ggc	192
Leu	Glu	Thr	Val	Leu	Thr	Ile	Leu	His	Ala	Gly	Gly	Lys	Phe	Gly	Gly	
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Gly	Gly	Tyr	Lys	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Val	Ser	Val	
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gtc	aac	gcc	ctc	tca	gaa	tat	gtc	gaa	gtc	acc	gtg	tgg	cgg	gaa	ggc	288
Val	Asn	Ala	Leu	Ser	Glu	Tyr	Val	Glu	Val	Thr	Val	Trp	Arg	Glu	Gly	
			85					90					95			
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Lys	Thr	His	Gln	Gln	Arg	Phe	Glu	Gln	Gly	Asn	Pro	Ile	Gly	Glu	Leu	
			100					105					110			
caa	gtt	gcc	ccg	gat	gcc	gac	gat	cgc	cgc	ggg	aca	caa	gtt	cgt	ttc	384
Gln	Val	Ala	Pro	Asp	Ala	Asp	Asp	Arg	Arg	Gly	Thr	Gln	Val	Arg	Phe	
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Arg	Ile	Asp	Phe	Thr	Asp	Glu	Arg	Leu	Gln	Leu	Thr	Lys	Asn	His	Glu		
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ccc	cat	caa	gaa	acc	tat	tac	ttt	gaa	ggc	ggc	att	cgc	gaa	tac	gtc	576	
Pro	His	Gln	Glu	Thr	Tyr	Tyr	Phe	Glu	Gly	Gly	Ile	Arg	Glu	Tyr	Val		
			180					185					190				
gcc	tac	atg	aat	acc	gat	aaa	cag	gcg	ctg	cac	tca	gag	att	atc	ttt	624	
Ala	Tyr	Met	Asn	Thr	Asp	Lys	Gln	Ala	Leu	His	Ser	Glu	Ile	Ile	Phe		
			195				200					205					
gtg	caa	tcc	gaa	aaa	gat	ggc	gtc	caa	gtt	gaa	gct	gca	ttg	caa	tgg	672	
Val	Gln	Ser	Glu	Lys	Asp	Gly	Val	Gln	Val	Glu	Ala	Ala	Leu	Gln	Trp		
			210				215					220					
tgc	gtt	gac	gcc	tac	agc	gac	aac	att	ctg	ggc	ttt	gcc	aac	aac	atc	720	
Cys	Val	Asp	Ala	Tyr	Ser	Asp	Asn	Ile	Leu	Gly	Phe	Ala	Asn	Asn	Ile		
225				230						235				240			
cgc	acg	att	gac	ggc	ggc	acc	cat	att	gag	ggg	ctc	aaa	act	gtt	ctg	768	
Arg	Thr	Ile	Asp	Gly	Gly	Thr	His	Ile	Glu	Gly	Leu	Lys	Thr	Val	Leu		
				245					250					255			
acg	cgg	acg	atg	aac	acg	atc	gcc	cgc	aaa	cgg	aat	aaa	cgc	aag	gat	816	
Thr	Arg	Thr	Met	Asn	Thr	Ile	Ala	Arg	Lys	Arg	Asn	Lys	Arg	Lys	Asp		
			260					265					270				
gcc	gac	aat	aac	ctg	tcg	ggc	gag	aat	att	cgc	gaa	ggg	tta	aca	gcg	864	
Ala	Asp	Asn	Asn	Leu	Ser	Gly	Glu	Asn	Ile	Arg	Glu	Gly	Leu	Thr	Ala		
			275				280					285					
atc	gtt	tcg	gtc	aaa	gtt	ccg	gat	ccg	gaa	ttt	gaa	ggg	caa	acc	aaa	912	
Ile	Val	Ser	Val	Lys	Val	Pro	Asp	Pro	Glu	Phe	Glu	Gly	Gln	Thr	Lys		
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[illegible]

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305

310

315

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Gly

325

330

335

1056

Leu

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345

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&lt;211

&lt;212

&lt;213

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Ile

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305	310	315
Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp		
325	330	335
Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala		
340	345	350
Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser		
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Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu		
370	375	380
Ser Glu Ile Phe Ile Val		
385	390	

[illegible]

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185

190

cgc gcg gcc ctg acc cgg atc atc acc agc tac gcc gag agc tcc ggc 624

Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly

195

200

205

atc ctg aag aag gaa aag gtc agc ctg ggc ggc gaa gac agc cgc gag 672

Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu

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25

30

Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser

35

40

45

Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala





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tgg aac gac agc ttc aac gag aac ctg ttg tgc ttc acc aac aac att	480
Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile	
145 150 155 160	
ccg cag cgc gat ggc ggt act cac ctg gtg ggt ttc cgt tcc gcc ctg	528
Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu	
165 170 175	
acg cgt aac ctc aat acg tat atc gaa gcc gaa ggc ctg gcg aag aag	576
Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys	
180 185 190	
cac aag gtc gcg acc acc ggt gac gat gcc cgt gaa ggc ctg gcc gcg	624
His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala	
195 200 205	
atc att tcg gta aaa gtg ccg gat ccg aag ttc agc tcc cag acc aag	672
Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys	
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gac aag ctg gtt tct tcc gaa gtg aag acc gcg gtc gaa cag gaa atg	720
Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met	
225 230 235 240	
ggc aag tac ttc tcc gac ttc ctg ctg gaa aac ccg aac gaa gcc aag	768
Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys	
245 250 255	
ctg gtt gtc ggc aag atg atc gac gcg gca cgt gct cgt gaa gcg gcg	816
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260 265 270	
cgc aag acc cgt gag atg acc cgc cgc aaa ggc gcg ctg gac atc gcc	864
Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala	



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Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe  
50 55 60  
Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu  
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Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg  
85 90 95  
Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe  
100 105 110  
Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His  
115 120 125  
Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln  
130 135 140

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 145 150 155 160  
 Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu  
 165 170 175  
 Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys  
 180 185 190  
 His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala  
 195 200 205  
 Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys  
 210 215 220  
 Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met  
 225 230 235 240  
 Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys  
 245 250 255  
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35

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Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg

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35 40 45

Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu

50 55 60

Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu

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Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser

85 90 95

Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp

100 105 110

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115

120

125

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130

135

140

Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg

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25

30

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40

45

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Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile	
85 90 95	
gtg acc aag atc gcc gag gcc gcc gcc gcc cgc gag gcc gcc cgc aag	336
Val Thr Lys Ile Ala Glu Ala Ala Ala Ala Arg Glu Ala Ala Arg Lys	
100 105 110	
gcg cga gag ctg acc cgc cgc aag agc gcg ctc gac atc acc agc ctg	384
Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu	
115 120 125	
ccc gcc aag ctc gcc gac tgc tgc gaa cgc gat ccg gcc aag tcc gag	432
Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu	
130 135 140	
atc ttc atc gtc gag ggc gac tgc gcg ggc ggc tgc gcc aag cag gcc	480
Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala	
145 150 155 160	
cgc aac cgc gac aac cag gcc gtt ctg ccc ctg cgc ggc aag atc ctg	528
Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu	
165 170 175	
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Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile	
180 185 190	
ggc acg ctg atc acc gcc ctg ggc gcg ggg atc ggc cgc gac gac ttc	624
Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe	

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65                      70                      75                      80  
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85                      90                      95  
Val Thr Lys Ile Ala Glu Ala Ala Ala Arg Glu Ala Ala Arg Lys  
100                      105                      110  
Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu  
115                      120                      125  
Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu  
130                      135                      140

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Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala  
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 165 170 175  
 Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile  
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 Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu  
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<211> 1422

<212> DNA

<213> Cytophaga lytica

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 Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg  
 20 25 30  
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 Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr



35	40	45	
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Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr			
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gaa acg ctt tct aac aga atg cga gag ttg gct tac ctt aat aag gga	288		
Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly			
85	90	95	
gtt aca att agc att aca gat aag aga gtt aaa gat gaa aag gga gag	336		
Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu			
100	105	110	
ttt tta tct gaa gtt ttt tac tct gaa gaa gga cta aaa gaa ttt att	384		
Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile			
115	120	125	
aag ttt tta gac ggt aac aga gaa caa cta ata cgt gat gtt gtt tca	432		
Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser			
130	135	140	
atg gaa ggt gaa aaa aac gga att cct gtt gag gtt gca atg gtg tac	480		
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr			
145	150	155	160
aat aca tca tat tca gaa aat ctt cac tct tac gta aat aat att aat	528		
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn			
165	170	175	
aca cat gaa ggt ggt aca cac ctt tca ggt ttt aga aga ggt tta aca	576		
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr			
180	185	190	
tca acc tta aaa aag tat gca gat gca tct gga atg tta gac aaa tta	624		

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Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu	
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Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile	
210	215
gtg tct gtt aaa gtt gca gaa cct cag ttt gaa ggg caa aca aaa act	720
Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr	
225	230
aaa tta ggt aac aga gaa gtt tct tct gca gtg agc caa gct gta tca	768
Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser	
245	250
gaa atg ctt acc aac tat tta gaa gaa aac cca gat gat gct aag gta	816
Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val	
260	265
att gta caa aaa gtc att tlg gca gcg caa gca cgt cat gcg gct aca	864
Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr	
275	280
aaa gcc cgt gaa atg gta cag cgt aaa acg gta atg agt ata ggt ggt	912
Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly	
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Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys	
305	310
gaa gta ttc ctt gta gag gga gat tgc gcg ggt ggt act gct aaa caa	1008
Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln	
325	330
ggt agg gac aga aac ttt cag gca ata tta ccg ctt cgt ggt aaa atc	1056
Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile	
340	345
	350



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Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val

1 5 10 15

Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg

20 25 30

Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr

35 40 45

Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr

50 55 60

Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr

65 70 75 80

Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly

85 90 95

Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu

100 105 110

Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile

115 120 125

Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser

130 135 140

Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr

145 150 155 160

Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn

165 170 175

Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr

180 185 190

Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu

195 200 205

Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile

00023629.033001



Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser

450

455

460

Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr

465

470

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His Ala Gly Gly Lys Phe Asp

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44

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Lys Val Pro Glu Pro Lys Phe

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Ala Arg Lys Ala Arg Glu

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<211> 19

<212> PRT

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<223> Xaa1 = Pro or Ser; Xaa2 = Ala or Thr; Xaa3 = Ala, Val or Leu; Xaa4 = Glu or Asp;  
Xaa5 = Val or Thr; Xaa6 = Ile or Val; Xaa7 = Met, Leu or Phe; Xaa8 = Val, Gln or Ile;  
Xaa9 = Asp or Gly; Xaa10 = Asp, Gly, Asn or Ser; Xaa11 = Ser, Lys, Gly, Asp or Asn

<400> 69

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Leu His Ala Gly Gly Lys Phe

1 5 10 15

Xaa Xaa Xaa

<210> 70

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<212> PRT

<213> Artificial Sequence

<400> 70

Gly Gly Thr His

1

0982389-033004

<210> 71

<211> 15

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Ile or Leu; Xaa2 = Ala or Ser

<400> 71

Xaa Met Thr Asp Ala Asp Val Asp Gly Xaa His Ile Arg Thr Leu

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5

10

15

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Gly or Ala; Xaa2 = Ser or Asp

<400> 72

Arg Lys Arg Pro Xaa Met Tyr Ile Gly Xaa Thr

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5

10

<210> 73

<211> 6

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Thr or Pro; Xaa2 = Lys or Asn; Xaa3 = Thr, Asp, Gly, Lys, Ser, Phe or Tyr

<400> 73

Gln Xaa Xaa Xaa Lys Leu

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<210> 74

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<400> 74

Xaa Lys Gly Leu Gly Glu Met Asn Xaa

1

5

<210> 75

<211> 9

<212> PRT

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<400> 75

Val Glu Gly Asp Ser Ala Gly Gly Ser

1

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<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = His or Val; Xaa2 = Gln or Lys

<400> 76

Lys Xaa Pro Asp Pro Xaa Phe

1

5

09623899.033001



<210> 80

<211> 7

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Pro or Asn; Xaa2 = Thr or Gln

<400> 80

Phe Thr Asn Asn Ile Xaa Xaa

1

5

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